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May 1, 2003

Ms. Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

Re: US Patent Application No. 09/870,353
For: IMPROVED NUCLEIC ACID MODIFYING ENZYMES
Inventors: Yan Wang, et al.
Filed: May 30, 2001
Our File No.: 020130-000111US

Dear Ms. Steele:

The enclosed replacement sequence listing diskette with paper copy and statement letter is being sent to you pursuant to our telephone conversation today. Please let me know if you need anything else. Thank you for your assistance.

Very truly yours,

A handwritten signature in black ink, appearing to read "Jean M. Lockyer".

Jean M. Lockyer, Ph.D.
Patent Agent

JML/mcd
Enclosure

SF 1456680 v1



I hereby certify that this is being send via "FedEx" on May 1, 2003
to:

Ms Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

PATENT
Attorney Docket No.: 020130-000111US

TOWNSEND and TOWNSEND and CREW LLP

By: Malinda C. Wright

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

WANG *et al.*

Application No.: 09/870,353

Filed: May 30, 2001

For: IMPROVED NUCLEIC ACID
MODIFYING ENZYMES

Examiner: Not yet assigned

Art Unit: 1633

SUBMISSION OF REPLACEMENT COPY
OF SEQUENCE LISTING

Ms Shirley Steele
U.S. Patent and Trademark Office
2011 South Clark Place
Crystal Plaza 2, Room 7D25
Arlington, VA 22202

Sir:

In response to the May 1, 2003 telephone request for a replacement copy of the computer readable form (CRF) of the Sequence Listing that was previously filed on August 5, 2002, Applicants submit herewith the requested replacement CFR and paper copy of the Sequence Listing.

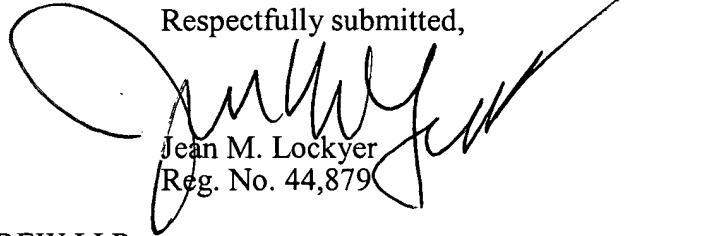
The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

WANG *et al.*
Application No.: 09/870,353
Page 2

PATENT

If it is believed that a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



Jean M. Lockyer
Reg. No. 44,879

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SF 1456614 v1



#12

SEQUENCE LISTING

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Xi, Lei
Prosen, Dennis E.
MJ Bioworks, Inc.

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Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile
			565					570						575	
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		580						585					590		
Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr
	595						600					605			
Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp
	610					615					620				
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625					630					635					640
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			645						650					655	

Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile		
			660					665					670				
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		675					680					685					
Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val		
		690				695					700						
Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe		
705				710					715					720			
Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys		
			725					730					735				
Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser		
		740						745					750				
Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg		
		755					760					765					
Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu		
	770					775					780						
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785				790					795					800			
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			805						810					815			
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Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu	Val	Met		
865					870				875					880			
Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Ile		
			885					890						895			
Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	Gly	Ile	Asp	Gly	Arg	Gly	Gly		
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 Pfu-Ssod7d

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 <223> Pfu-Ssod7d

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 aagattgtga gaattgttga tgtagagaag gttgagaaaa agtttctcgg caagcctatt 240
 accgtgtgga aactttattt ggaacatccc caagatgttc ccactattag agaaaaagtt 300
 agagaacatc cagcagttgt ggacatcttc gaatacgata ttccatttgc aaagagatac 360
 ctcatcgaca aaggcctaata accaatggag ggggaagaag agctaaagat tcttgccttc 420
 gatatatgaaa ccctctatca cgaaggagaa gagtttggaa aaggcccaat tataatgatt 480
 agttatgcag atgaaaatga agcaaaggtg attacttggg aaaacataga tcttccatac 540
 gttgaggttg tatcaagcga gagagagatg ataaagagat ttctcaggat tatcaggagg 600

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atgcagagaa taggcgatat gacggctgta gaagtcagg gaagaatata tttcgacttg 780
tatcatgtaa taacaaggac aataaatctc ccaacatata cactagaggc tgtatatgaa 840
gcaatttttg gaaagccaaa ggagaaggta tacgccgacg agatagcaaa agcctgggaa 900
agtggagaga accttgagag agttgccaaa tactcgatgg aagatgcaaa ggcaacttat 960
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tacatcgagt tagtatggaa ggagctcgaa gaaaagtttg gatttaaagt cctctacatt 1620
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ctcgcaatat atgagcagat aacaagacca ttacatgagt ataaggcgat aggtcctcac 2040
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ggatacatag tacttagagg cgatggtcca attagcaata gggcaattct agctgaggaa 2160
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gcggtactta ggatattgga gggatttggg tacagaaagg aagacctcag atacaaaaag 2280
acaagacaag tcggcctaac ttcttgggtt aacattaaaa aatccggtac cggcggtggc 2340
ggtgcaaccg taaagttcaa gtacaaaggc gaagaaaaag aggtagacat ctccaagatc 2400
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aagcagaaaa agtga 2535

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<210> 8
<211> 844
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:fusion protein
      Pfu-Ssod7d

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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
      35             40             45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
      50             55             60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
      65             70             75             80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
      85             90             95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
      100            105            110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
      115            120            125

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145					150					155					160
Ser	Tyr	Ala	Asp	Glu	Asn	Glu	Ala	Lys	Val	Ile	Thr	Trp	Lys	Asn	Ile
				165					170					175	
Asp	Leu	Pro	Tyr	Val	Glu	Val	Val	Ser	Ser	Glu	Arg	Glu	Met	Ile	Lys
				180				185					190		
Arg	Phe	Leu	Arg	Ile	Ile	Arg	Glu	Lys	Asp	Pro	Asp	Ile	Ile	Val	Thr
				195			200					205			
Tyr	Asn	Gly	Asp	Ser	Phe	Asp	Phe	Pro	Tyr	Leu	Ala	Lys	Arg	Ala	Glu
	210				215						220				
Lys	Leu	Gly	Ile	Lys	Leu	Thr	Ile	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys
225					230					235					240
Met	Gln	Arg	Ile	Gly	Asp	Met	Thr	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile
				245					250					255	
His	Phe	Asp	Leu	Tyr	His	Val	Ile	Thr	Arg	Thr	Ile	Asn	Leu	Pro	Thr
			260					265					270		
Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Lys	Pro	Lys	Glu
		275					280					285			
Lys	Val	Tyr	Ala	Asp	Glu	Ile	Ala	Lys	Ala	Trp	Glu	Ser	Gly	Glu	Asn
	290					295					300				
Leu	Glu	Arg	Val	Ala	Lys	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Ala	Thr	Tyr
305					310					315					320
Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ile	Gln	Leu	Ser	Arg	Leu
				325					330					335	
Val	Gly	Gln	Pro	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu
			340					345					350		
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Val	Ala
		355					360					365			
Pro	Asn	Lys	Pro	Ser	Glu	Glu	Glu	Tyr	Gln	Arg	Arg	Leu	Arg	Glu	Ser
	370					375					380				
Tyr	Thr	Gly	Gly	Phe	Val	Lys	Glu	Pro	Glu	Lys	Gly	Leu	Trp	Glu	Asn
385					390					395					400
Ile	Val	Tyr	Leu	Asp	Phe	Arg	Ala	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr
				405					410					415	
His	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Leu	Glu	Gly	Cys	Lys	Asn	Tyr
			420					425					430		
Asp	Ile	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Ile	Pro	Gly
		435					440					445			
Phe	Ile	Pro	Ser	Leu	Leu	Gly	His	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Ile
	450					455				460					
Lys	Thr	Lys	Met	Lys	Glu	Thr	Gln	Asp	Pro	Ile	Glu	Lys	Ile	Leu	Leu
465					470					475					480
Asp	Tyr	Arg	Gln	Lys	Ala	Ile	Lys	Leu	Leu	Ala	Asn	Ser	Phe	Tyr	Gly
				485					490					495	
Tyr	Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu
			500					505					510		
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		515					520					525			
Leu	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ile	Asp	Thr	Asp	Gly
	530					535					540				
Leu	Tyr	Ala	Thr	Ile	Pro	Gly	Gly	Glu	Ser	Glu	Glu	Ile	Lys	Lys	Lys
545					550					555					560
Ala	Leu	Glu	Phe	Val	Lys	Tyr	Ile	Asn	Ser	Lys	Leu	Pro	Gly	Leu	Leu
				565					570					575	
Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys
			580					585					590		
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly
		595					600						605		

Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln
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Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala
625						630				635					640
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile
				645					650					655	
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His
			660					665					670		
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala
		675					680					685			
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val
	690					695					700				
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu
705					710					715					720
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn
				725					730					735	
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg
			740					745					750		
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser
		755					760					765			
Trp	Leu	Asn	Ile	Lys	Lys	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Ala	Thr	Val
	770					775					780				
Lys	Phe	Lys	Tyr	Lys	Gly	Glu	Glu	Lys	Glu	Val	Asp	Ile	Ser	Lys	Ile
785					790					795					800
Lys	Lys	Val	Trp	Arg	Val	Gly	Lys	Met	Ile	Ser	Phe	Thr	Tyr	Asp	Glu
				805					810					815	
Gly	Gly	Gly	Lys	Thr	Gly	Arg	Gly	Ala	Val	Ser	Glu	Lys	Asp	Ala	Pro
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<210> 9
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:fusion protein
 Sac7d-deltaTaq

<220>
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<210> 10
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 Sac7d-deltaTaq

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			20					25					30		
Lys	Met	Val	Ser	Phe	Thr	Tyr	Asp	Asp	Asn	Gly	Lys	Thr	Gly	Arg	Gly
		35					40					45			
Ala	Val	Ser	Glu	Lys	Asp	Ala	Pro	Lys	Glu	Leu	Leu	Asp	Met	Leu	Ala
	50					55					60				
Arg	Ala	Glu	Arg	Glu	Lys	Lys	Gly	Gly	Gly	Val	Thr	Ser	Pro	Lys	Ala
	65				70					75				80	
Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe
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Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	Glu	Pro	Tyr	Lys	Ala
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Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ser
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Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	Pro	Gly	Asp	Asp	Pro
	145				150					155					160
Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly
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Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	Ala	Gly	Glu	Arg
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Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	Trp	Gly	Arg	Leu	Glu
		195				200						205			
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	210					215					220				
Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg	Leu	Asp	Val
225					230					235					240

Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	Glu	Glu	Ile	Ala	Arg
				245					250					255	
Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn
			260					265					270		
Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Gly	Leu	Pro
		275					280					285			
Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala
	290					295					300				
Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu
	305				310					315					320
Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	Ile	Asp	Pro	Leu
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Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn
			340					345					350		
Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu
		355				360						365			
Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala
	370					375					380				
Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln
	385				390					395					400
Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile
				405					410					415	
Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	Thr	Ala	Ser	Trp
			420				425						430		
Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala
		435					440					445			
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg
	450					455					460				
Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile
	465				470					475					480
Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys
				485					490					495	
Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly
			500					505					510		
Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg
		515					520					525			
Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala
	530					535						540			
Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Glu
	545				550					555					560
Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp	Glu	Leu	Val	Leu
				565					570					575	
Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu
			580				585						590		
Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val
		595					600					605			
Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	Gly	Ile	Asp	Gly	Arg
	610					615					620				
Gly	Gly	Gly	Gly	His	His	His	His	His	His						
625					630										

<210> 11

<211> 1965

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein
PL-deltaTaq

<220>
 <221> CDS
 <222> (1)..(1965)
 <223> PL-deltaTaq

<400> 11
 atgattacga attcgaagaa aaagaaaaag aaaaagcgta agaaacgcaa aaagaaaaag 60
 aaaggcggcg gtgtcactag tggcgcaacc gtaaagttca agtacaaagg cgaagaaaaa 120
 gaggtagaca tctccaagat caagaaagta tggcgtgtgg gcaagatgat ctccctcacc 180
 tacgacgagg gcggtggcaa gaccggccgt ggtgcggtaa gcgaaaagga cgcgccgaag 240
 gagctgctgc agatgctgga gaagcagaaa aaggcgggcg gtgtcaccag tcccaaggcc 300
 ctggaggagg cccctggcc cccgccggaa ggggccttcg tgggctttgt gctttcccg 360
 aaggagccca tgtgggccga tcttctggcc ctggccgccc ccaggggggg cgggtccac 420
 cgggcccccg agccttataa agcctcagg gacctgaagg aggcgcgggg gcttctcgcc 480
 aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgccccg cgacgacccc 540
 atgctcctcg cctacctcct ggaccttcc aacaccacc ccgagggggg ggccggcgcc 600
 tacggcgggg agtggacgga ggaggcgggg gagcggggcg ccctttccga gaggctcttc 660
 gccaacctgt gggggaggct tgagggggag gagaggctcc tttggcttta ccgggagggtg 720
 gagaggcccc tttccgctgt cctggccac atggaggcca cgggggtgcg cctggacgtg 780
 gcctatctca gggccttgct cctggagggt gccgaggaga tcgcccgcct cgaggccgag 840
 gtcttccgct tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc 900
 ctctttgacg agctagggt tcccgccatc ggcaagacgg agaagaccgg caagcgctcc 960
 accagcgccg ccgtcctgga ggccctccgc gaggccacc ccatcgtgga gaagatcctg 1020
 cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc 1080
 caccacagga cgggccgcct ccacaccgc ttcaaccaga cggccacggc cacgggcagg 1140
 ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg 1200
 atccgcccgg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag 1260
 atagagctca ggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag 1320
 gagggcgggg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc 1380
 gtggaccccc tgatgcgccg ggcggccaag acctcaact tcggggctcct ctacggcatg 1440
 tcggcccccac gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt 1500
 gagcgctact ttcagagctt cccaagggtg cgggcctgga ttgagaagac cctggaggag 1560
 ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagacct 1620
 gagggccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgct 1680
 cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag 1740
 gaaatggggg ccaggatgct ccttcagggt cacgacgagc tggtcctcga ggccccaaaa 1800
 gagagggcgg aggcctggc ccggctggcc aaggagggtc tggagggggg gtatcccctg 1860
 gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc 1920
 attgatggcc gcggcggagg cgggcacatc catcatcatc attaa 1965

<210> 12
 <211> 654
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: fusion protein
 PL-deltaTaq

<400> 12
 Met Ile Thr Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg
 1 5 10 15
 Lys Lys Lys Lys Lys Gly Gly Gly Val Thr Ser Gly Ala Thr Val Lys
 20 25 30
 Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
 35 40 45
 Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
 50 55 60
 Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
 65 70 75 80

Glu	Leu	Leu	Gln	Met	Leu	Glu	Lys	Gln	Lys	Lys	Gly	Gly	Gly	Val	Thr	85	90	95
Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	100	105	110
Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	Leu	115	120	125
Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	Glu	130	135	140
Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	Ala	145	150	155
Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	Pro	165	170	175
Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	180	185	190
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Glu	195	200	205
Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	Trp	210	215	220
Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	Val	225	230	235
Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	245	250	255
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	Glu	260	265	270
Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	275	280	285
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	290	295	300
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	305	310	315
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	325	330	335
Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	Tyr	340	345	350
Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	His	355	360	365
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	370	375	380
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	385	390	395
Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	Leu	405	410	415
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	420	425	430
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Glu	435	440	445
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	450	455	460
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	465	470	475
Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	485	490	495
Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	500	505	510
Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	515	520	525
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	530	535	540
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	545	550	555

Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe
				565					570					575	
Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp
			580					585					590		
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg
		595					600					605			
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu
	610					615					620				
Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu	Gly
625					630					635					640
Ile	Asp	Gly	Arg	Gly	Gly	Gly	Gly	His	His	His	His	His	His		
				645				650							

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L71F

<400> 13
 cctgctctgc cgcttcacgc 20

<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L71R

<400> 14
 gcacagcggc tggctgagga 20

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L18015F

<400> 15
 tgacggagga taacgccagc ag 22

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer L23474R

<400> 16
 gaaagacgat gggtcgctaa tacgc 25

<210> 17
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L18015F

 <400> 17
 tgacggagga taacgccagc ag 22

<210> 18
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L29930R

 <400> 18
 ggggttgagg gtcaatgggt tc 22

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L30350F

 <400> 19
 cctgctctgc cgcttcacgc 20

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L35121R

 <400> 20
 cacatggtac agcaagcctg gc 22

<210> 21
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L2089F

 <400> 21
 cccgtatctg ctgggatact ggc 23

<210> 22
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L7112R

 <400> 22
 cagcgggtgct gactgaatca tgg 23

 <210> 23
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L30350F

 <400> 23
 cctgcctgcc gcttcacgc 19

 <210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer L40547R

 <400> 24
 ccaatacccg tttcatcgcg gc 22

 <210> 25
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer
 H-Amelo-Y

 <400> 25
 ccacctcatc ctgggcacc 19

 <210> 26
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial
 Sequence:primerH-Amelo-YR

 <400> 26
 gcttgaggcc aaccatcaga gc 22

<210> 27
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 beta-globin primer Bglbn536F

 <400> 27
 ggttggccaa tctactccca gg 22

 <210> 28
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 beta-globin primer Bglbn536R

 <400> 28
 gctcactcag tgtggcaaag 20

 <210> 29
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:human
 beta-globin primer Bglbn1408R

 <400> 29
 gattagcaaa agggcctagc ttgg 24

 <210> 30
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:6-His epitope
 tag

 <400> 30
 His His His His His His
 1 5

 <210> 31
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:anti-DYKDDDDK
 epitope tag

<400> 31
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 32
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 32
Gly Gly Val Thr
1

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 33
Gly Thr Gly Gly Gly Gly
1 5

<210> 34
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:lysine-rich
peptide

<400> 34
Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys
1 5 10 15
Gly Gly Gly Val Thr
20